REMARKS

Claim 1 has been amended to label the two formulae "(I)" and "(II)" for convenience of reference, and to incorporate the functional limitations of claims 3-4 on the peptide sequence of formula (I) and the compound itself. This in turn mooted claims 3-4 (now cancelled) and the functional limitation of claim 11 (now deleted).

We wish to point out to the examiner that the three amino acid types referred to in claim 1 (hydrophobic, basic, acidic) are defined at P18, L17-21.

Claim 11 also has been amended to strike the sequences not included in the alignment attached to the election with traverse, as well as sequences which do not satisfy the requirement of a basic AA (SID 11, 12, 14, 38-46, 51, 53, 56-58, 60, 61, 63, 65, 68, 72, 98) or of Gly/Ala (SID 22, 23).

Minor grammatical or spelling corrections have been made to claims 15, 16 and 20.

Claims 11, 17-19 spokes of fragments that "have" a particular sequence. The word "have" can be interpreted as either open (like "comprising") or closed (like "consists of"). We have amended 17-19 to replace "have" with "consist(s) of", but added claims 35-37 which instead recite "comprising".

Claim 1 contemplates a compound comprising two individual peptide sequences, "at least one" of which comprises the sequence of formula (I). The implication of "at least one" is that in some embodiments they both satisfy it, hence new claim 38. The possibilities of two SID 1, two SID 2, or SID 1 + SID 2 are set forth in new claims 35-37.

The "fragment" language, defined at P28, L19-22, has been excised from claims 11, 12 and 14 and instead new claim 39 recites that the compound comprises at least 9 consecutive amino acids of SEQ ID NO:1 or 2. Basis is at P20, L8-11 and P20 L34-P21, L2.

The "variant" and "homologue" language, defined at P25,

L25-P26, L4 has been excised from claims 11, 12 and 14, and
new claims have been presented:

40: at least 50% positive amino acid matches with SID1
(P25, L25).

41: at least 60% positive amino acid matches with SID1
(P26, L12-P27, L10; P33, L7-P34, L4).

42: at least 90% positive (ditto).

43: SID1-8 (P26, L2-12). (SID 1-9 are in the defined
group 1. However SID 9 is omitted from the claim because it
is not in the aforementioned alignment.)

44: at least 90% identical to SID 1.

Claim 13 is cancelled in favor of new claim 43.

We have compared the motif requirements to elected
species SID1 and 2, with these results:

	Residue Positions	
Requirement	SID1	SID2
hydrophobic AA (L/I/V/F/W/Y)	2, 3, 4, 5	2, 4, 5, 6, 12, 16
basic AA (R/K/H)	12, 14	14, 15
acidic (D/E)/N/Q	1, 7, 8, 9, 10	1, 3, 7, 9, 10
G/A	6, 11, 15	8, 11, 13

It can be seen that the shortest fragment of SID1 that
satisfies the motif is AA 5-12 (VAENQQGK), and the shortest
such fragment of SID2 is AA 10-14 (NALGK).

When the sequence has more than one of the required types
of amino acids, it is arbitrary which of the compliant
positions is said to provide it. Hence SID1 and 2 together
imply the following preferred sequence satisfying the motif of
claim 1

$X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8$
wherein

at least one of X_1 and X_6 is hydrophobic;

at least one of X_2, X_5 and X_7 is Gly or Ala;

at least one of X_3, X_4, X_5 and X_6 is acidic, Asn or Gln; and

X_8 is basic.

SID1 and 2 both also satisfy the rule

(D/E/N/Q)-3 aa-(R/K/H)

and in particular

N-(3 aa)-K.

They also have in common the more extensive sequence

(A/G)-(D/E/N/Q)-(D/E/N/Q)-(2aa)-(A/G)-(R/K/H)

and in particular

AEN -(2aa)-GK (SEQ ID NO:147).

These observations are reflected in new claims 45-49.

Please note that the sequence listing has not yet been revised to include SEQ ID NO:147. If claim 49, reciting SID 147, is deemed acceptable, we will submit a revised sequence listing. If it is rejected, we may decide to cancel 48 which would then moot the need to revise the sequence listing.

All of the new claims read on the elected subject matter.

Respectfully submitted,

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